

17. Hashed

1652

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/367,013A
DATE: 08/01/2000
TIME: 16:10:58

Input Set : A:\Cgabl.app
Output Set: N:\CRF3\08012000\I367013A.raw

see
P. 5, 700

3 <110> APPLICANT: KNUTZON, DEBORAH
4 MUKERJI, PRADIP
5 HUANG, YUNG-SHENG
6 THURMOND, JENNIFER
7 CHAUDHARY, SUNITA
8 LEONARD, AMANDA E.
10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN
11 POLYUNSATURATED FATTY ACIDS
13 <130> FILE REFERENCE: CGAB-210 USA
15 <140> CURRENT APPLICATION NUMBER: 09/367,013A
16 <141> CURRENT FILING DATE: 1999-08-05
18 <150> PRIOR APPLICATION NUMBER: 08/834,655
19 <151> PRIOR FILING DATE: 1997-04-11
21 <160> NUMBER OF SEQ ID NOS: 40
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1617
27 <212> TYPE: DNA
28 <213> ORGANISM: Mortierella alpina
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
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35 acaacaaacc atggctgctg ctcccagtggt gaggacgttt actcggggcg aggttttgaa 120
36 tgccgaggct ctgaatgagg gcaagaagga tgccgaggca cccttcttga tgatcatcga 180
37 caacaagggt tacgatgtcc gcgagttcgt ccctgatcat cccgggtgaa gtgtgattct 240
38 caccgacgtt ggcaaggacg gcaactgacgt ctttgacact ttacaccccg aggtctgctt 300
39 ggagactctt gccaaactttt acgttggtga tattgacgag agcgaccgcg atatcaagaa 360
40 tgatgacttt gcggccgagg tccgcaagct gcgtaccttg ttccagtctc ttggttacta 420
41 cgattcttcc aaggcatact acgccttcaa ggtctcgttc aacctctgca tctgggggtt 480
42 gtcgacggtc atttggtcca agtggggcca gacctcgacc ctgcaccaac tgctctcgcc 540
43 tgcgcttttg ggtctgttct ggcagcagtg cggatgggtg gctcagcact ttttgcatca 600
44 ccagggtcttc caggaccgtt tctgggggtg tcttttcggc gccttcttgg gaggtgtctg 660
45 ccagggtcttc tctgctcgtt ggttgaagga caagcacaac actcaccacg cggcccccac 720
46 cgtccacggc gaggatcccg acattgacac ccacctctg ttgacctgga gtgagcatgc 780
47 gttggagatg ttctcggatg tcccagatga ggagctgacc cgcattgtgt cgcgtttcat 840
48 ggtcctgaac cagacctggt tttacttccc cattctctcg ttgcccgtc tctcctggtg 900
49 cctccagtc attctctttg tgctgcctaa cggtcaggcc cacaagccct cgggcgcgcg 960
50 tgtgcccatc tctgttgctg agcagctgtc gcttgcgatg cactggacct ggtacctcgc 1020
51 caccatgttc ctgttcatca aggatcccggt caacatgctg gtgtactttt tgggtgtcga 1080
52 ggcgggtgtc ggaacttgtt tggcgatcgt gttctcgtc aaccacaacg gtatgcctgt 1140
53 gatctcgaag gaggaggcgg tcgatatgga ttcttccacg aagcagatca tcacgggtcg 1200
54 tgatgtccac ccgggtctat ttgccaactg gttcacgggt ggattgaact atcagatcga 1260
55 gcaccacttg ttcccttcga tgctcgcga caacttttca aagatccagc ctgctgtcga 1320
56 gacctgtgac aaaaagtaca atgtccgata ccacaccacc ggtatgatcg agggaaactg 1380
57 agagggtctt agcgtctga acgaggtctc caaggctgcc tccaagatgg gtaaggcgca 1440
58 gtaaaaaaaa aaacaaggac gtttttttcc gccagtgctc gtgcctgtgc ctgcttccct 1500

← no response shown.

Response is mandatory
when sequence
is combined DNA/RNA.

see 1.823 of
New Sequence
Revised

RECEIVED
JUG-9 2000
TC 1500 MAIL ROOM

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59 tgtcaagtcg agcgtttctg gaaaggatcg ttcagtgcag tatcatcatt ctccttttac 1560
60 cccccgctca tatctcattc atttctctta ttaaacaact tgttcccccc ttcaccg 1617
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 457
65 <212> TYPE: PRT
66 <213> ORGANISM: Mortierella alpina
68 <400> SEQUENCE: 2
69 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
70 1 5 10 15
72 Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
73 20 25 30
75 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
76 35 40 45
78 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
79 50 55 60
81 Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
82 65 70 75 80
84 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
85 85 90 95
87 Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
88 100 105 110
90 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
91 115 120 125
93 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
94 130 135 140
96 Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
97 145 150 155 160
99 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
100 165 170 175
102 His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
103 180 185 190
105 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
106 195 200 205
108 His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
109 210 215 220
111 Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
112 225 230 235 240
114 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
115 245 250 255
117 Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
118 260 265 270
120 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
121 275 280 285
123 Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
124 290 295 300
126 Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
127 305 310 315 320
129 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
130 325 330 335

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132 Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His
133          340          345          350
135 Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
136          355          360          365
138 Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
139          370          375          380
141 Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
142 385          390          395          400
144 Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
145          405          410          415
147 Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
148          420          425          430
150 Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
151          435          440          445
153 Ala Ala Ser Lys Met Gly Lys Ala Gln
154          450          455
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 1488
159 <212> TYPE: DNA
160 <213> ORGANISM: Mortierella alpina
162 <400> SEQUENCE: 3
163 gtccctgtc gctgtcgga caccatcc tccctgctc cctctcggtt tgtccttggc 60
164 ccacgtctc tctccaccc tccgagacga ctgcaactgt aatcaggaac cgacaaatac 120
165 acgatttctt tttactcagc accaactcaa aatcctcaac cgcaaccctt tttcaggatg 180
166 gcacctccca acactatcga tgcgggtttg acccagcgtc atatcagcac ctcggcccca 240
167 aactcgccca agcctgcctt cgagcgcaac taccagctcc ccgagttcac catcaaggag 300
168 atccgagagt gcatccctgc ccactgcttt gagcgctccg gtctccgtgg tctctgccac 360
169 gttgccatcg atctgacttg ggcgtcgctc ttgttcttgg ctgcgacca gatcgacaag 420
170 tttgagaatc ccttgatccg ctatttggcc tggcctgttt actggatcat gcagggtatt 480
171 gtctgcaccg gtgtctgggt gctggctcac gagtgtggtc atcagtcctt ctcgacctcc 540
172 aagacctca acaacacagt tggttggatc ttgcaactga tgccttgggt cccctaccac 600
173 tctggagaa tctcgcactc gaagcaccac aaggccactg gccatatgac caaggaccag 660
174 gtctttgtgc ccaagaccg ctcccagggt ggcttgctc ccaaggagaa cgctgctgct 720
175 gccgttcagg aggaggacat gtccgtgcac ctggatgagg aggtcccat tgtgactttg 780
176 ttctggatgg tgatccagtt ctgttcgga tggcccgctg acctgattat gaacgcctct 840
177 ggccaagact acggccgctg gacctcgcac ttccacacgt actgcacctt ctttgagccc 900
178 cgcaactttt tcgacattat tatctcggac ctcggtgtgt tggctgccct cggcgccctg 960
179 atctatgcct ccattgcagt gtctgtcttg accgtcacca agtactatat tgtcccctac 1020
180 ctctttgtca acttttgggt ggtcctgac acccttcttg agcacaccga tcccagctg 1080
181 cccattacc gcgaggggtg ctggaatttc cagcggtggag ctctttgcac cgttgaccgc 1140
182 tcgttttgga agttcttggg ccataatgtt caccgcatg tccacacca tgtggcccat 1200
183 cacttggtct cgcaaatgcc gttctaccat gctgaggaag ctacctatca tctcaagaaa 1260
184 ctgctgggag agtactatgt gtacgacca tccccgatcg tcgttgcggt ctggaggctg 1320
185 ttccgtgagt gccgattcgt ggagatcag ggagacgtgg tctttttcaa gaagtaaaaa 1380
186 aaaagacaat ggaccacaca caacctgtgc tctacagacc tacgtatcat gtagccatac 1440
187 cacttcataa aagaacatga gctctagagg cgtgtcattc gcgcctcc 1488
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 399
192 <212> TYPE: PRT

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193 <213> ORGANISM: Mortierella alpina
195 <400> SEQUENCE: 4
196 Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
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199 Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
200 20 25 30
202 Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
203 35 40 45
205 His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
206 50 55 60
208 Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Thr Gln Ile Asp
209 65 70 75 80
211 Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
212 85 90 95
214 Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
215 100 105 110
217 Cys Gly His Gln Ser Phe Ser Thr Lys Thr Leu Asn Asn Thr Val
218 115 120 125
220 Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
221 130 135 140
223 Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Thr Lys Asp
224 145 150 155 160
226 Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
227 165 170 175
229 Glu Asn Ala Ala Ala Val Gln Glu Glu Asp Met Ser Val His Leu
230 180 185 190
232 Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
233 195 200 205
235 Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
236 210 215 220
238 Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
239 225 230 235 240
241 Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
242 245 250 255
244 Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
245 260 265 270
247 Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
248 275 280 285
250 Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
251 290 295 300
253 Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
254 305 310 315 320
256 Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
257 325 330 335
259 Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
260 340 345 350
262 Glu Glu Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
263 355 360 365
265 Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu

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266      370      375      380
268 Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
269 385      390      395
272 <210> SEQ ID NO: 5
273 <211> LENGTH: 355
274 <212> TYPE: PRT
275 <213> ORGANISM: Mortierella alpina
277 <400> SEQUENCE: 5
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279 1 5 10 15
281 Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile
282 20 25 30
284 Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
285 35 40 45
287 Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
288 50 55 60
290 Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
291 65 70 75 80
293 Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
294 85 90 95
296 Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
297 100 105 110
299 Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
300 115 120 125
302 Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
303 130 135 140
305 Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
306 145 150 155 160
308 Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
309 165 170 175
311 Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser
312 180 185 190
314 Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
315 195 200 205
317 His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
318 210 215 220
320 Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
321 225 230 235 240
323 Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
324 245 250 255
326 Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
327 260 265 270
329 Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
330 275 280 285
332 Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
333 290 295 300
335 His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
336 305 310 315 320
338 Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu

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Full
↓

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Cgabl.app

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L:360 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:360 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:360 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:366 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:366 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:444 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:444 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:444 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:447 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:447 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:465 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:465 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:493 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:493 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:493 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:558 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:558 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:558 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:726 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
L:726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
L:726 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
L:736 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:736 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:736 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:743 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
M:340 Repeated in SeqNo=21
L:744 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
L:744 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:744 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:744 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:757 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:757 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
L:757 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
L:760 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
L:760 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
M:340 Repeated in SeqNo=22
L:1173 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34

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Input Set : A:\Cgabl.app

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L:1173 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1173 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:1176 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1176 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:1182 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1182 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1185 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
L:1185 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:34
L:1232 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1232 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:1232 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
L:1235 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1235 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
M:340 Repeated in SeqNo=35
L:1238 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:35
L:1238 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:35
L:1272 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:1330 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
L:1401 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:1529 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
M:340 Repeated in SeqNo=39
L:1684 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
M:340 Repeated in SeqNo=40